

## ERROR DETECTED: SUGGESTED CORRECTION

SERIAL NUMBER: 09/143,482

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3, as this will prevent "wrapping".
- 2 ☐ **Wrapped Amino Acids** The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing to align the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES." response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ **Use of <213>Organism (NEW RULES)** Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 ☒ **Use of <220>Feature (NEW RULES)** Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown". Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.



AK3-Diotechnology Systems Branch, 5/15/99

502

JO09 Rec'd PCT  
BIOTECHNOLOGY  
SYSTEMS  
BRANCH

21 FEB 2001 CT

**RAW SEQUENCE LISTING  
ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/743,482  
Source: PCT 09  
Date Processed by STIC: 2-15-01

5040

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER. 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX. 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin31help@uspto.gov](mailto:patin31help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER  
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED  
FEB 28 2001  
OPE JCS

Does Not Comply  
Corrected Dikette Needed

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/743,482DATE: 02/15/2001  
TIME: 13.47.33Input Set: A:\ES.txt  
Output Set: N:\CRF3\02152001\1\43482.raw

3 <110> APPLICANT: Lonnen GmbH  
5 <120> TITLE OF INVENTION: Immunological reagent specifically interacting with the  
6 extracellular domain of the human sctg chain  
8 <130> FILE REFERENCE: C1368PCT  
-> 10 <140> CURRENT APPLICATION NUMBER: US/09/743,482  
-> 11 <141> CURRENT FILING DATE: 2001-02-02  
12 <150> PRIOR APPLICATION NUMBER: EP 98 11 2867.1  
14 <151> PRIOR FILING DATE: 1998-07-10  
16 <160> NUMBER OF SEQ ID NOS: 18  
18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

365 <210> SEQ ID NO: 18  
366 <211> LENGTH: 332  
367 <212> TYPE: PRT  
368 <213> ORGANISM: Artificial Sequence  
370 <220> FEATURE:  
371 <223> OTHER INFORMATION: Description of Artificial Sequence: artificial  
372 sequence  
374 <400> SEQUENCE: 18  
375 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
376 1 5 10 15  
378 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala  
379 20 25 30  
381 Ser Pro Gln Glu Ile Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile  
382 35 40 45  
384 Gly Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln  
385 50 55 60  
387 Leu Leu Ile Tyr Ser Ala Thr Ser Leu Ala Asp Gly Ile Pro Ser Arg  
388 65 70 75 80  
390 Phe Ser Gly Ser Arg Ser Gly Thr Gln Tyr Ser Leu Lys Ile Ser Arg  
391 85 90 95  
393 Leu Gln Val Glu Asp Thr Gly Ile Tyr Tyr Cys Leu Gln Arg Tyr Ser  
394 100 105 110  
396 Asn Pro Asn Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly  
397 115 120 125  
399 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gln Val Gln  
400 130 135 140  
402 Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ser Ser Val Lys  
403 145 150 155 160  
405 Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asp Met His  
406 165 170 175  
408 Trp Ile Lys Glu Cln Pro Gly Asn Gly Leu Glu Trp Ile Gly Trp Ile  
409 180 185 190  
411 Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Gln Lys Phe Asn Gly Lys

Non-valid response  
too vague. What  
is the source of  
the artificial  
sequence?

See #12 on the  
Error Summary  
Sheet.

Note:  
Seq #17 is also  
errored in this  
way. Please review  
and correct.

C:\Cr3\Outhold\Vsrl743482.htm

2/15/01

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/743,482

DATE: 02/15/2001  
TIME: 15:47:33

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02152001\743482.raw

```

412      195      200      205
414 Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu
415      210      215      220
417 Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Asp
418 225      230      235      240
420 Trp His Tyr Tyr Ser Ser Tyr Ile Arg Pro Phe Ala Tyr Trp Gly Gln
421      245      250      255
423 Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Clu Val Gln
424      260      265      270
426 Leu Leu Glu Gln Ser Gly Ala Clu Leu Ala Arg Pro Gly Ala Ser Val
427      275      280      285
429 Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Leu
430      290      295      300
432 Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp Ile Gly Glu
433 305      310      315      320
435 Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys Phe Lys Gly
436      325      330      335
438 Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Ser Met Gln
439      340      345      350
441 Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
442      355      360      365
444 Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp Val Trp Gly
445      370      375      380
447 Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
448 385      390      395      400
450 Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Cln Thr Pro
451      405      410      415
453 Leu Ser Leu Pro Val Ser Leu Gly Asp Cln Ala Ser Ile Ser Cys Arg
454      420      425      430
456 Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp
457      435      440      445
459 Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
460      450      455      460
462 Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
463 465      470      475      480
465 Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Clu Ala Clu Asp Leu
466      485      490      495
468 Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly
469      500      505      510
471 Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Thr Ser His His His His
472      515      520      525
474 His His Thr Ser
475      530
-> 479 1

```

Please delete the extraneous numeral  
at the end of the file. It is causing  
an invalid amino acid count for  
sequence #18.

e://C:\CrF3\Outhold\Vsrf743482.htm

2/15/01



# Raw Sequence Listing Error Summary

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